

## FULL LENGTH APO-A1 SEQUENCE

1  
MKA AVL TLAVL FLTGSQARHFWQQDEPPQSPWDRVKDLATVYVD  
VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE  
TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE  
LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL<sup>194</sup>RQRLAARLEALKENG GARLAEYHA  
KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ<sup>267</sup> (SEQ ID NO:2)

sig\_peptide 20..91  
mature\_protein 92..820

20 a tgaaagctgc ggtgctgacc ttggccgtgc tcttcctgac  
61 ggggagccag gctcggcatt tctggcagca agatgaaccc cccagagcc cctgggatcg  
121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt  
181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg  
241 ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga  
301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct  
361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga  
421 ggagatggag ctctaccgcc agaaggtgga gccgctgcgc gcagagctcc aagagggcgc  
481 gcgccagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga  
541 ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gcccctaca gcgacgagct  
601 gcgccagcgc ttggccgcgc gccttgaggc tctcaaggag aacggcggcg ccagactggc  
661 cgagtaccac gccaaggcca ccgagcatct gagcacgctc agcgagaagg ccaagcccgc  
721 gctcgaggac ctccgccaag gcctgctgcc cgtgctggag agcttcaagg tcagcttcct  
781 gagcgtctc gaggagtaca ctaagaagct caacaccag (SEQ ID NO:1)

**FIG. 1A**

## 18K N-TERMINAL FRAGMENT

25

DEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE

TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE

LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL (SEQ ID NO:3)<sup>194</sup>

92 gatgaaccc cccagagcc cctgggatcg

121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt

181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg

241 ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga

301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct

361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga

421 ggagatggag ctctaccgcc agaaggtgga gccgctgcgc gcagagctcc aagagggcgc

481 gcgccagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga

541 ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgagct

601 g (SEQ ID NO:4)

**FIG. 1B**

13K N-TERMINAL FRAGMENT

25

DEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLG PVTQEFWDNLEKE

TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE<sup>144</sup> (PORTION OF  
SEQ ID NO:3)

92 gatgaaccc cccagagcc cctgggatcg

121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt

181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg

241 ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctgggcctg tgaccagga

301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct

361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga

421 ggagatggag ctctaccgcc agaaggtgga g (PORTION OF SEQ ID NO:4)

**FIG. 1C**

## 13K C-TERMINAL FRAGMENT

156

QKLHE

LQEKLSPLGEEMRD RARAHVDALRTHLAPYSDEL<sup>194</sup>RQRLAARLEALKENG GARLA EYHA  
KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ<sup>267</sup> (PORTION OF  
SEQ ID NO:2)

485 cagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga

541 ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgagct

601 gcgccagcgc ttggccgcgc gccttgaggc tctcaaggag aacggcggcg ccagactggc

661 cgagtaccac gccaaggcca ccgagcatct gagcacgctc agcgagaagg ccaagcccgc

721 gctcgaggac ctccgccaag gcctgctgcc cgtgctggag agcttcaagg tcagcttcct

781 gagcgtcttc gaggagtaca ctaagaagct caacacccag (PORTION OF SEQ ID NO:1)

**FIG. 1D**